A. Kubelik●

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OIPE

RAW SEQUENCE LISTING   DATE: 08/16/2001
PATENT APPLICATION: US/09/596,958   TIME: 13:17:19

Input Set : A:\C32861.app
Output Set: N:\CRF3\08162001\I596958.raw

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 3 <110> APPLICANT: Kim, Jihyun Francis
 4        Beer, Steven V.
 6 <120> TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM ERWINIA AMYLOVORA
 7        AND ITS USE
 9 <130> FILE REFERENCE: 19603/3286
11 <140> CURRENT APPLICATION NUMBER: 09/596,958
12 <141> CURRENT FILING DATE: 2000-06-20
14 <150> PRIOR APPLICATION NUMBER: 09/120,927
15 <151> PRIOR FILING DATE: 1998-07-22
17 <150> PRIOR APPLICATION NUMBER: 60/055,108
18 <151> PRIOR FILING DATE: 1997-08-06
20 <160> NUMBER OF SEQ ID NOS: 3
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1344
26 <212> TYPE: DNA
27 <213> ORGANISM: Erwinia amylovora
29 <400> SEQUENCE: 1
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32 cggcaaacca ttgagcaaat ggctcaatta ttggcggaac tgttaaagtc actgctatcg 180
33 ccacaatcag gtaatgcggc aaccggagcc ggtggcaatg accagactac aggagttggt 240
34 aacgctggcg gcctgaacgg acgaaaaggc acagcaggaa ccactccgca gtctgacagt 300
35 cagaacatgc tgagtgagat gggcaacaac gggctggatc aggccatcac gcccgatggc 360
36 cagggcggcg ggcagatcgg cgataatcct ttactgaaag ccatgctgaa gcttattgca 420
37 cgcatgatgg acggccaaag cgatcagttt ggccaacctg gtacgggcaa caacagtgcc 480
38 tcttccggta cttcttcatc tggcggttcc ccttttaacg atctatcagg ggggaaggcc 540
39 ccttccggca actccccttc cggcaactac tctcccgtca gtaccttctc acccccatcc 600
40 acgccaacgt ccccctacctc accgcttgat ttcccttctt ctcccaccaa agcagccggg 660
41 ggcagcacgc cggtaaccga tcatcctgac cctgttggta gcgcgggcat cggggccgga 720
42 aattcggtgg ccttcaccag cgccggcgct aatcagacgg tgctgcatga caccattacc 780
43 gtgaaagcgg gtcaggtgtt tgatggcaaa ggacaaacct tcaccgccgg ttcagaatta 840
44 ggcgatggcg gccagtctga aaaccagaaa ccgctgttta tactggaaga cggtgccagc 900
45 ctgaaaaacg tcaccatggg cgacgacggg gcggatggta ttcatcttta cggtgatgcc 960
46 aaaatagaca atctgcacgt caccaacgtg ggtgaggacg cgattaccgt taagccaaac 1020
47 agcgcgggca aaaaatccca cgttgaaatc actaacagtt ccttcgagca cgcctctgac 1080
48 aagatcctgc agctgaatgc cgatactaac ctgagcgttg acaacgtgaa ggccaaagac 1140
49 tttggtactt ttgtacgcac taacggcggt caacagggta actgggatct gaatctgagc 1200
50 catatcagcg cagaagacgg taagttctcg ttcgttaaaa gcgatagcga ggggctaaac 1260
51 gtcaatacca gtgatatctc actgggtgat gttgaaaacc actacaaagt gccgatgtcc 1320
52 gccaacctga aggtggctga atga                                    1344
55 <210> SEQ ID NO: 2
56 <211> LENGTH: 447
57 <212> TYPE: PRT
58 <213> ORGANISM: Erwinia amylovora
60 <400> SEQUENCE: 2
61 Met Ser Ile Leu Thr Leu Asn Asn Asn Thr Ser Ser Ser Pro Gly Leu
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62   1                5                    10                     15
64 Phe Gln Ser Gly Gly Asp Asn Gly Leu Gly Gly His Asn Ala Asn Ser
65            20                    25                     30
67 Ala Leu Gly Gln Gln Pro Ile Asp Arg Gln Thr Ile Glu Gln Met Ala
68            35                    40                     45
70 Gln Leu Leu Ala Glu Leu Leu Lys Ser Leu Leu Ser Pro Gln Ser Gly
71        50                    55                     60
73 Asn Ala Ala Thr Gly Ala Gly Gly Asn Asp Gln Thr Thr Gly Val Gly
74  65                    70                    75                     80
76 Asn Ala Gly Gly Leu Asn Gly Arg Lys Gly Thr Ala Gly Thr Thr Pro
77                85                    90                     95
79 Gln Ser Asp Ser Gln Asn Met Leu Ser Glu Met Gly Asn Asn Gly Leu
80            100                   105                    110
82 Asp Gln Ala Ile Thr Pro Asp Gly Gln Gly Gly Gly Gln Ile Gly Asp
83            115                   120                    125
85 Asn Pro Leu Leu Lys Ala Met Leu Lys Leu Ile Ala Arg Met Met Asp
86        130                   135                    140
88 Gly Gln Ser Asp Gln Phe Gly Gln Pro Gly Thr Gly Asn Asn Ser Ala
89 145                   150                   155                    160
91 Ser Ser Gly Thr Ser Ser Ser Gly Gly Ser Pro Phe Asn Asp Leu Ser
92                165                   170                    175
94 Gly Gly Lys Ala Pro Ser Gly Asn Ser Pro Ser Gly Asn Tyr Ser Pro
95            180                   185                    190
97 Val Ser Thr Phe Ser Pro Pro Ser Thr Pro Thr Ser Pro Thr Ser Pro
98            195                   200                    205
100 Leu Asp Phe Pro Ser Ser Pro Thr Lys Ala Ala Gly Gly Ser Thr Pro
101        210                   215                    220
103 Val Thr Asp His Pro Asp Pro Val Gly Ser Ala Gly Ile Gly Ala Gly
104 225                   230                   235                    240
106 Asn Ser Val Ala Phe Thr Ser Ala Gly Ala Asn Gln Thr Val Leu His
107                245                   250                    255
109 Asp Thr Ile Thr Val Lys Ala Gly Gln Val Phe Asp Gly Lys Gly Gln
110            260                   265                    270
112 Thr Phe Thr Ala Gly Ser Glu Leu Gly Asp Gly Gly Gln Ser Glu Asn
113            275                   280                    285
115 Gln Lys Pro Leu Phe Ile Leu Glu Asp Gly Ala Ser Leu Lys Asn Val
116        290                   295                   300
118 Thr Met Gly Asp Asp Gly Ala Asp Gly Ile His Leu Tyr Gly Asp Ala
119 305                   310                   315                    320
121 Lys Ile Asp Asn Leu His Val Thr Asn Val Gly Glu Asp Ala Ile Thr
122            325                   330                   335
124 Val Lys Pro Asn Ser Ala Gly Lys Lys Ser His Val Glu Ile Thr Asn
125            340                   345                   350
127 Ser Ser Phe Glu His Ala Ser Asp Lys Ile Leu Gln Leu Asn Ala Asp
128        355                   360                   365
130 Thr Asn Leu Ser Val Asp Asn Val Lys Ala Lys Asp Phe Gly Thr Phe
131        370                   375                   380
133 Val Arg Thr Asn Gly Gly Gln Gln Gly Asn Trp Asp Leu Asn Leu Ser
134 385                   390                   395                    400
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```

```
136 His Ile Ser Ala Glu Asp Gly Lys Phe Ser Phe Val Lys Ser Asp Ser
137             405             410             415
139 Glu Gly Leu Asn Val Asn Thr Ser Asp Ile Ser Leu Gly Asp Val Glu
140             420             425             430
142 Asn His Tyr Lys Val Pro Met Ser Ala Asn Leu Lys Val Ala Glu
143         435             440             445
146 <210> SEQ ID NO: 3
147 <211> LENGTH: 31
148 <212> TYPE: DNA
149 <213> ORGANISM: Erwinia amylovora
151 <220> FEATURE:
152 <221> NAME/KEY: unsure
153 <222> LOCATION: (8)
154 <223> OTHER INFORMATION: n at any position is unknown
156 <400> SEQUENCE: 3
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W--> 157 cggaaccnnn ncnnnnnnnn nnccactcaa t   31

VERIFICATION SUMMARY   DATE: 08/16/2001
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L:157 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3